

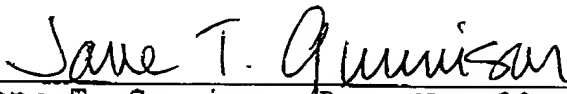
Remarks

The July 10, 2001 Communication stated that the amendments to the specification filed on April 20, 2001 were not entered because a marked-up copy showing the changes to the specification required by 37 C.F.R. § 1.121 was missing.

Accordingly, applicant hereby submits marked-up copies of specification pages 11 and 12 entitled "Version with markings to show changes made" showing changes that have been made. The underlining marking on these marked-up copies indicates addition of text.

Applicants request that the Examiner enter the amendments to the specification, and allow the pending claims to issue.

Respectfully submitted,



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Version with markings to show changes made"

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TABLE 2

5	1.	AGTCTAGTCTTATCTTGTATGTGTCCTGCACT..GA..ACTTGTTTCTGT
	2.	AGTCTAGTTTCATTCTGTGTGTGTTTGGCACT..GA..AATTATTTCTGT
	3.	AGTTTGGTTCTCTCTTGAGTGTGTTTGTGTT..AG..CATAATTTCTGT
	4.	TGACAGG.GTTATTTTCACC.TCTTCTT..TTCTACTCCACAG.TG.T.T
	5.	TGACAGG.GTTATTTTCACC.TCTTCTCTCTTCTACTTCATAG.TG.T.T
	6.	AGGCCGGTGTGCGTTTGTCTATATGTTATTTTCCAC..CATA.TTGCCGT
10	1.	CTCTGGAGTGCTCTACACTTCAGTAGGGGCTGT.A.CCCGGGCGGTCCCA
	2.	CTCTGGGGTGCTTTACACTTCAGTAGGGGCTGT.A.CCCGGGCGGTCCCA
	3.	CTCTAGAGTGCTTTACACTCTAGTAGGGGCTGT.A.CCCGGGCGGTCCCA
	4.	CT.A.....TACTGTG..GAAGGGTATGTGT....TGCCCCCTTCCT
	5.	CT.A.....TACTATG.AA.AGGGTATGTGT..C..GCCCTTCCT
	6.	CT.T.....TTGGCAATGT.G.AGGGCCCG.GAAACCTGGCCCTGTCT
20	1.	CTCTTCACAGGAATCTGCACAGGTGGCTTTTAC.CTCTGGACAGTGCATT
	2.	CTCTTCACAGGAATNTGCACAGGTGGCTTTTAC.CTCTGGACAGTGCATT
	3.	CTCTTCACAGGAATCTGCACAGGTGGCTTTTAC.CTCTGGACAGTGCATT
	4.	.TCTTGAGAAACGT..GCGCGGCGGTCTTTCCGTCTCTCGACAA.GCGC.
	5.	.TCTTGAGAAACGT..GCGTGCGCGGTCTTTCCGTCTCTCGAAAAACG..T
	6.	.TCTTGACGAGCAT.T.CCTAGGGGTCTTTCCC.CTCTCGCCAAAGGAAT
25	1.	CCACACCCG.C.TCCACGGTAGAAGATGATGTGTGTCTTTGCT..TGTGA
	2.	CCACACCCG.C.TCCACAGTAGAAGATGATGTGTGTCTTTGCT..TGTGA
	3.	CCATACCCG.C.TCCACAATAGAAGATGATGTATATCTTTGTT..TGTGA
	4.	GCGT..GCAACATACAGAGT.AACG.CGAAGAA.AGCA..GTTC.TC.GG
	5.	GCGT..GCGACATGCAGAGT.AACG.CAAAGAA.AGCA..GTTC.T.TGG
	6.	GCA.A.G.GTC.TGTTGAAT.GTCG.TGAAGGA.AGCA..GTTCCTCTGG
30	1.	AAA.GCTT...GTGAAAATC.....GTGTGTAGGCGTAGCGGCTACT
	2.	AAA.GCTT...GTGAAAATC.....GTGTGTAGGCGTAGCGGNTACT
	3.	AAT.GCT.CA..TGAA.A.C.....GTGTGTGTAGGCGTAGCGGCTACT
	4.	TCTAGCT.CTAGTGCCCA.CAAGAAAACAGCTGTAG.CG.ACCA.C.ACA
	5.	TCTAGCT.CTGGTGCCCA.CAAGAAAACAGCTGTAG.CG.ACCA.C.ACA
	6.	AA..GCTTCT..TGAAGA.CAA.ACAACGTCTGTAG.CG.ACC..CT..T
35	1.	TGAGTGCCAGCGGATTACCCCTAGTGGTAACTAGC [SEQ ID NO: 1]
	2.	TGAGTGCCAGCGGACNACCCCTAGTGGTAACTAGC [SEQ ID NO: 2]
	3.	TGAATGCCAGCGGAACCCCTAGTGGTAACTAGC [SEQ ID NO: 3]
	4.	..AAGGC.AGCGGAACCCCTCTGTTAACTAGGAGC [SEQ ID NO: 5]
	5.	..AAGGC.AGCGGAACCCCTCTGTTAACTAGGAGC [SEQ ID NO: 6]
	6.	TGCAGGC.AGCGGAACCCCTCTGTTAACTAGGAGC [SEQ ID NO: 7]
40	1.	TGAGTGCCAGCGGATTACCCCTAGTGGTAACTAGC [SEQ ID NO: 1]
	2.	TGAGTGCCAGCGGACNACCCCTAGTGGTAACTAGC [SEQ ID NO: 2]
	3.	TGAATGCCAGCGGAACCCCTAGTGGTAACTAGC [SEQ ID NO: 3]
	4.	..AAGGC.AGCGGAACCCCTCTGTTAACTAGGAGC [SEQ ID NO: 5]
	5.	..AAGGC.AGCGGAACCCCTCTGTTAACTAGGAGC [SEQ ID NO: 6]
	6.	TGCAGGC.AGCGGAACCCCTCTGTTAACTAGGAGC [SEQ ID NO: 7]
45	1.	TGAGTGCCAGCGGATTACCCCTAGTGGTAACTAGC [SEQ ID NO: 1]
	2.	TGAGTGCCAGCGGACNACCCCTAGTGGTAACTAGC [SEQ ID NO: 2]
	3.	TGAATGCCAGCGGAACCCCTAGTGGTAACTAGC [SEQ ID NO: 3]
	4.	..AAGGC.AGCGGAACCCCTCTGTTAACTAGGAGC [SEQ ID NO: 5]
	5.	..AAGGC.AGCGGAACCCCTCTGTTAACTAGGAGC [SEQ ID NO: 6]
	6.	TGCAGGC.AGCGGAACCCCTCTGTTAACTAGGAGC [SEQ ID NO: 7]

In this region of the viral genome, Ljungan 174F has 94% homology to Ljungan 87-012 (here taken as the indicator strain for comparisons), and Ljungan 145SL

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has 91% homologous residues to Ljungan 87-012. The TMEBeAn strain has 69%, Vilyuisk has 68% and EMCV has 68% homologous residues to Ljungan 87-012. Using the same criteria for calculating the homology, EMCV has 85% homology to TMEBeAn.

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Table 3 shows alignment of cDNA sequences from the polyprotein coding sequences of the Ljungan 145SL isolate [SEQ ID NO. 4] to the amino acid sequences of sequenced cardioviruses in the comparative alignment compiled by Dr. A. Palmenberg (personal comm.)^{*} The TMEBeAn strain was arbitrarily taken as the indicator strain, while the amino acids of the remaining strains are shown only if they differ from the indicator strain. For the Ljungan 145SL isolate, similar, but non-identical amino acids are indicated in small type. The amino acid homology between Ljungan 145SL and other cardioviruses was established screening the entire Swiss Protein Data Bank using the BLITZ search algorithm with standard search parameters.

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^{*} Table 3 shows the alignment of Ljungan 145SL [SEQ ID NO. 4], TMEBeAn [SEQ ID NO. 8], TMEGd7 [SEQ ID NO. 9], TMEGdz6 [SEQ ID NO. 10], TMEDA [SEQ ID NO. 11], Vilyuisk [SEQ ID NO. 12], EMCBD [SEQ ID NO. 13], EMCBC [SEQ ID NO. 14], EMCDD [SEQ ID NO. 15], EMCDC [SEQ ID NO. 16], EMCV1 [SEQ ID NO. 17], EMCR [SEQ ID NO. 18], MengoM [SEQ ID NO. 19] and Mengo37a [SEQ ID NO. 20].